Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (previously presented) An isolated polynucleotide comprising at least about 17 consecutive nucleotides of SEQ ID NO:1 including residue 2285, where residue 2286 has an A to C substitution; or comprising at least about 17 consecutive nucleotides of SEQ ID NO:1 including residue 3281, where residue 3282 has a T to G substitution; or comprising at least about 25 consecutive nucleotides of SEQ ID NO:1 including residue 2285, where residue 2286 has an A to C substitution; or comprising at least about 25 consecutive nucleotides of SEQ ID NO:1 including residue 3281, where residue 3282 has a T to G substitution; or comprising at least about 40 consecutive nucleotides of SEQ ID NO:1 including residue 2285, where residue 2286 has an A to C substitution; or comprising at least about 40 consecutive nucleotides of SEQ ID NO:1 including residue 3281, where residue 3282 has a T to G substitution.

2. (previously presented) Isolated genetic material from human Chromosome 5 of an individual that indicates the presence of dyslexia or a predisposition to develop dyslexia in the individual from whom the material was obtained, the material comprising a sufficient portion of SEQ ID NO:1 comprising (Haplotype #1) an A to T substitution at residue 879 and a G to A substitution at residue 2613; or comprising (Haplotype #2) an A to C substitution at residue 424, a C to A substitution at residue 554, a C to T substitution at residue 1346, an A to C substitution at residue 2286, a G to A substitution at residue 2314 and a G to A substitution at residue 2613; or comprising (Haplotype #3) a G to A substitution at residue 1145 and a G to A substitution at residue 2613; or (Haplotype #4) comprising an A to C substitution at residue 424, a C to A substitution at residue 554, a C to T substitution at residue 1346, a G to A substitution at residue 2314, a G to A substitution at residue 2613 and a T to G substitution at residue 3282; or comprising (Haplotype #5) an A to C substitution at residue 424, a C to A

substitution at residue 554, an A to T substitution at residue 879, a C to T substitution at residue 1346, a G to A substitution at residue 2314, a G to A substitution at residue 2613 and a T to G substitution at residue 3282; or comprising (Haplotype #6) an A to T substitution at residue 879; or comprising (Haplotype #7) an A to C substitution at residue 2286 and a G to A substitution at residue 2613; where except for these substitutions, residue 424 is A, residue 554 is C, residue 879 is A, residue 985 is C, residue 1145 is G, residue 1346 is C, residue 2275 is A, residue 2286 is A, residue 2314 is G, residue 2453 is C, residue 2613 is G, residue 3282 is T.

3. (currently amended) A method of diagnosing dyslexia or a predisposition to develop dyslexia, the method comprising:

a) providing a sample from an individual containing genetic material from Chromosome 5; and

b) analyzing the genetic material for the presence of one or more than one of ~~the isolated polynucleotide of claim 1~~ an isolated polynucleotide comprising at least about 17 consecutive nucleotides of SEQ ID NO:1 including residue 2285, where residue 2286 has an A to C substitution; or comprising at least about 17 consecutive nucleotides of SEQ ID NO:1 including residue 3281, where residue 3282 has a T to G substitution; or comprising at least about 25 consecutive nucleotides of SEQ ID NO:1 including residue 2285, where residue 2286 has an A to C substitution; or comprising at least about 25 consecutive nucleotides of SEQ ID NO:1 including residue 3281, where residue 3282 has a T to G substitution; or comprising at least about 40 consecutive nucleotides of SEQ ID NO:1 including residue 2285, where residue 2286 has an A to C substitution; or comprising at least about 40 consecutive nucleotides of SEQ ID NO:1 including residue 3281, where residue 3282 has a T to G substitution, or ~~Haplotype #1 through Haplotype #7 according to claim 2~~ isolated genetic material from human Chromosome 5 of an individual that indicates the presence of dyslexia or a predisposition to develop dyslexia in the individual from whom the material was obtained, the material comprising a sufficient portion of SEQ ID NO:1 comprising (Haplotype #1) an A to T

substitution at residue 879 and a G to A substitution at residue 2613; or comprising (Haplotype #2) an A to C substitution at residue 424, a C to A substitution at residue 554, a C to T substitution at residue 1346, an A to C substitution at residue 2286, a G to A substitution at residue 2314 and a G to A substitution at residue 2613; or comprising (Haplotype #3) a G to A substitution at residue 1145 and a G to A substitution at residue 2613; or (Haplotype #4) comprising an A to C substitution at residue 424, a C to A substitution at residue 554, a C to T substitution at residue 1346, a G to A substitution at residue 2314, a G to A substitution at residue 2613 and a T to G substitution at residue 3282; or comprising (Haplotype #5) an A to C substitution at residue 424, a C to A substitution at residue 554, an A to T substitution at residue 879, a C to T substitution at residue 1346, a G to A substitution at residue 2314, a G to A substitution at residue 2613 and a T to G substitution at residue 3282; or comprising (Haplotype #6) an A to T substitution at residue 879; or comprising (Haplotype #7) an A to C substitution at residue 2286 and a G to A substitution at residue 2613; where except for these substitutions, residue 424 is A, residue 554 is C, residue 879 is A, residue 985 is C, residue 1145 is G, residue 1346 is C, residue 2275 is A, residue 2286 is A, residue 2314 is G, residue 2453 is C, residue 2613 is G, residue 3282 is T;

where the presence of the isolated polynucleotide ~~of claim 1~~ or of one or more than one of Haplotype #1 through Haplotype #7 indicates a diagnosis of dyslexia or a predisposition to develop dyslexia.

4. (previously presented) A method of diagnosing dyslexia or a predisposition to develop dyslexia, the method comprising:

a) providing a sample from an individual containing genetic material from Chromosome 5; and

b) analyzing the sample for the presence of one or more genetic variant that decreases the amount or activity of a gene product of the SNAJA gene, SEQ ID NO:1, as compared with the amount of the gene product or the amount of gene product activity for non-dyslexics;

where the presence of the variant of the gene indicates a diagnosis of dyslexia or a predisposition to develop dyslexia.

5. (previously presented) The method of claim 4, where analyzing the sample comprises contacting the sample with a polynucleotide probe complimentary to the mRNA of a variant form of SNAJA, SEQ ID NO:1, known to produce a decreased amount of gene product or a gene product having decreased activity.

6. (previously presented) A method of diagnosing dyslexia or a predisposition to develop dyslexia, the method comprising:

a) providing a sample from an individual potentially containing a gene product of SNAJA, SEQ ID NO:1; and

b) analyzing the sample to determine the amount or activity or both of the gene product of SNAJA, SEQ ID NO:1 as compared with the amount or activity or both of the gene product for non-dyslexics;

where the presence of a decreased amount or activity or both of the gene product indicates a diagnosis of dyslexia or a predisposition to develop dyslexia.

7. (previously presented) The method of claim 6, where analyzing the sample comprises contacting the sample with antibodies to thegene product of SNAJA, SEQ ID NO:1.

8. (previously presented) The method of claim 6, where the gene product is selected from the group consisting of SEQ ID NO:10 and SEQ ID NO:11.

9. (presently amended) The method of ~~any of claims 3 through 8~~ claim 3, where the sample is obtained *in utero* or post-mortem.

10. (presently amended) The method of ~~any of claims 3 through 8~~ claim 3, additionally comprising administering phonological testing to the individual to confirm the diagnosis of dyslexia.

11. (presently amended) The method of ~~any of claims 3 through 8~~ claim 3, additionally comprising analyzing genetic material from the individual for the presence of one or more than

one genetic marker for dyslexia or for a predisposition to develop dyslexia on a chromosome other than Chromosome 5 to confirm the diagnosis of dyslexia.

12. (previously presented) The method of claim 11, where the chromosome other than Chromosome 5 is selected from the group consisting of Chromosomes 1p, 2p, 3p, 3q, 4q, 6p21.3, 6q, 8p, 9p, 11p; 13q, 15q, 18p, 18p11.2, 21q, and Xq.

13. (previously presented) The method of claim 11, where the chromosome other than Chromosome 5 is selected from the group consisting of Chromosomes 6p21.3 and 18p11.2.

14. (presently amended) A method of ameliorating the symptoms of dyslexia or preventing dyslexia in an individual, the method comprising:

a) diagnosing dyslexia or a predisposition to develop dyslexia in the individual according to the method of ~~any of claims 3 through 13~~ claim 3; and

b) treating the individual.

15. (previously presented) The method of claim 14, where treating the individual comprises administering phonological training to the individual.

16. (presently amended) A method of classifying a dyslexic individual or group of dyslexic individuals, the method comprising:

a) diagnosing dyslexia or a predisposition to develop dyslexia in the individual or individuals according to the method of ~~any of claims 3 through 13~~ claim 3; and

b) assigning a classification to the individual or individuals based on the variant or haplotype identified as a result of the diagnosis.

17. (previously presented) A kit for diagnosing dyslexia or a predisposition to develop dyslexia designed to identify the presence of a polynucleotide according to claim 1, or the presence of one or more than one Haplotype #1 through Haplotype #7 ~~of claim 2~~, the kit comprising one or more than one primer selected from the group consisting of SEQ ID NO:2 through SEQ ID NO:9.

18. (previously presented) The kit of claim 17, further comprising one or more than one agent, substance or material selected from the group consisting of a PCR buffer, a thermostable DNA polymerase and dNTPs.

19. (previously presented) A cDNA that encodes a gene product of SNAJA, SEQ ID NO:1.

20. (previously presented) The cDNA of claim 19, selected from the group consisting of SEQ ID NO:12 and SEQ ID NO:13.